

Thu May 22 10:43:43 2003

seq1-seql5.res

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq1-seql5.res made by mruhl on Thu May 22 10:27:45-PDT.

Query sequence being compared: US-08-973-363-1 (1-723)
Number of sequences searched: 18
Number of scores above cutoff: 18

Results of the initial comparison of US-08-973-363-1 (1-723) with:
File: US08973363.seq

100-
N -
D 50-
M -
B -
E -
R -
O -
F 10-
S -
S -
Q 5-
Q -
U -
E -
N -
C -
S -
S -
SCORE 0 80 161 241 321 402 482 562 643 723
STDEV 1 1 1 2 3 4

PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 5.00 Window size 500
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
61 19 165.77
Times: CPU
00:00:00.00 Total Elapsed
00:00:00.00

Number of residues: 10306
Number of sequences searched: 18
Number of scores above cutoff: 18

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name Description Length Score Score Init. Opt.

1. US-08-973-363-1 Sequence 1, Application US 723 723 723 3.99 0
The list of other best scores is:

Sequence Name Description Length Score Score Init. Opt.

2. US-08-973-363-15 Sequence 15, Application 1316 62 169 0.01 0

1. US-08-973-363-1 (1-723)
US-08-973-363-1 Sequence 1, Application US/08973363

Initial Score = 723 Optimized Score = 723 Significance = 3.99
Residue Identity = 100% Matches = 723 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
CCCGTCGGAGGTTTCAGGAATGACTAGATGGGCACTTAGTCCCATGGTGTAGTACAAAGGTGATGGTT
|||||
X 10 20 30 40 50 60 70
CCCGTCGGAGGTTTCAGGAATGACTAGATGGGCACTTAGTCCCATGGTGTAGTACAAAGGTGATGGTT
|||||
80 90 100 110 120 130 140
GGTCAAAAGTTGGACTCGATGATCTCAGAGTCTTTCAGCCCTTAATAATCTATGAATCTGTAAATTTA
|||||
80 90 100 110 120 130 140
GGTCAAAAGTTGGACTCGATGATCTCAGAGTCTTTCAGCCCTTAATAATCTATGAATCTGTAAATTTA
|||||
150 160 170 180 190 200 210
TTCTTGATCTTTTGGAGCAAGTTTGGGATTTTGGTTCCTGTCACCTGTTCTTCTTCTTCTG
|||||
150 160 170 180 190 200 210
TTCTTGATCTTTTGGAGCAAGTTTGGGATTTTGGTTCCTGTCACCTGTTCTTCTTCTTCTG
|||||
220 230 240 250 260 270 280
AACTGACTTTTCATTTGCAACATGAGAAATGCTGATTTGTCAGGTTACAGCTAGTCACTGCTCTTGA
|||||
220 230 240 250 260 270 280
AACTGACTTTTCATTTGCAACATGAGAAATGCTGATTTGTCAGGTTACAGCTAGTCACTGCTCTTGA
|||||
290 300 310 320 330 340 350 360
AGTAGTGAGAAACATTTAGGGAATACCTGGAGTGAAGCAACAGCTGGTCTGCAACTGAGCTTTGGG
|||||
290 300 310 320 330 340 350 360
AGTAGTGAGAAACATTTAGGGAATACCTGGAGTGAAGCAACAGCTGGTCTGCAACTGAGCTTTGGG
|||||
370 380 390 400 410 420 430
ATTTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTGCTTCCATTAATGTTG
|||||
370 380 390 400 410 420 430
ATTTGAGAGCCACAGAGTGTATATAATTTGTTAATGATATCTGCTGCTTCCATTAATGTTG
|||||
440 450 460 470 480 490 500
TTTTATGAACCACTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT
|||||
440 450 460 470 480 490 500
TTTTATGAACCACTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT
|||||
510 520 530 540 550 560 570
ATTTAGAGCAGATGCGAGCACTAGGAGTCTGTGATGACAGCTGACAGCTGATGATTTTCTGATTA
|||||
510 520 530 540 550 560 570
ATTTAGAGCAGATGCGAGCACTAGGAGTCTGTGATGACAGCTGACAGCTGATGATTTTCTGATTA
|||||
580 590 600 610 620 630 640
AACTATGAGAGTGAACAGAAATCTGAGCTAGTTTCTTGGCTGACGTGAAATTTTGTGAGAAATTTTC
|||||
580 590 600 610 620 630 640
AACTATGAGAGTGAACAGAAATCTGAGCTAGTTTCTTGGCTGACGTGAAATTTTGTGAGAAATTTTC
|||||
650 660 670 680 690 700 710 720
AAGACTACATTAGTTGTTGTTGAGGAAATAAATGTTTAAAGTTGTCCTTCTTGAACCTCCCGACC

|||||
AAGACTACATTAGTTGTGTGTTGAGGAAATATAAATGTTAGTTGTCTCATTCTTGAACCTCCGACC
650 660 670 680 690 700 710 720

x
GGG
|||
GGG
x

2. US-08-973-363-1 (1-723)
US-08-973-363-15 Sequence 15, Application US/08973363

Initial Score = 62 Optimized Score = 169 Significance = 0.01
Residue Identity = 32% Matches = 174 Mismatches = 364
Gaps = 3 Conservative Substitutions = 0

140 150 160 170 180 x 190 200
TCTCTAATTTTATCTTGATCTTTTGGCGAAGTTGTTGGGATTTTGGTTTCCCTGTCACTGT
|||
ATTTATCGGCTAGTCACAAAAG
x 10 20

210 220 230 240 250 260 270
TTCTTTTCCCTTGAACTGACTTTTCATTGCAACATGAGAAATGCTGTATTGTCAGGTTACAAGTAGTCAA
|||
GATCAGTAGAAGAGATATTCTTGAAGAGCCCAAGAAAGATGTTAGTCAATTTAGTGTTCAGAGAA
30 40 50 60 70 80 90

280 290 300 310 320 330 340
TGGCTGCTTAGAGTAGTGAGAAACATTTAGGGAAATPACTGGAGTGAAGCAACACACAGTGGTACTGCCAAAC
|||
TGGACACACAGAGGAAACTGTACTACATACAGGCTCTACTCTTCAAGCTCAACACCTTTTAAATAAGGAAG
100 110 120 130 140 150 160

350 360 370 380 390 400 410 420
TGTAGCTTTGGGATTTGAGAGCCACAGAGTTGTATATAATTTGTTAATGATATCTGCCCTGCTTCC
|||
AGTTATCAGCAATTTTCAAGTTTGGTCTGAGGAACCTTTTAAAGAACCTGGAANNNGAAGAGAGAGCCCTC
170 180 190 200 210 220 230

430 440 450 460 470 480 490
ATTAATGCTGTGTTTATGAACACCTCTTTTGTGTTTGGCTTCTTCATATCCTGCTGTTGTA
|||
AGGAGATGATATAGATGAATCTGAGAGGCTGAACTCGAGAAATGAGTCAGGCCCATTAACCTGTAG
240 250 260 270 280 290 300 310

500 510 520 530 540 550 560
ATGAGTTAATGCAATTTAGAAGCACATGGCAGAACTAGGAGATCTGTGGATGACAGTGGTACAGGAGCTCTGA
|||
GAGATGAGTTTACTTTACAGTTCAAGTAGTAACTTTTCCATATGATGAAGATGACATTGAA---TTGG
320 330 340 350 360 370

570 580 590 600 610 620 630
ATTTTGTAGATAAATATGAGAGTGAAGAACTGAGGCTAGTTCTTGTAGCTGACTGTAATTTTGT
|||
AAACAGAAACAAATCTAAGAACTGGAAGAAATCATTCAGAAATTCAGTGGCGAGCAATAGAGGGGNGG
380 390 400 410 420 430 440 450

640 650 660 670 680 690 700
GAGAATATTTCAAGACTACATTAGTTGTGTTGAGGAAATAAATGTTTAAGTTCTCCATTCCTTGA
|||
AAAGACAAAGAACTTGAAGAAATATATATGCTTCCAGAAATGAGAACTGTCCAAACAGATCAGCTTTA
460 470 480 490 500 510 520

710 720 x
AACCTCCGACCGG
|||
ATGGAATGAAGGAGATGAGTGAAGAGATATCTGGATCTGTAGTGAATCCATCTCA
530 540 550 560 570 580


```
2240      2250      2260      2270      2280      2290      2300
2310      2320      2330      2340      2350      2360      2370
GAAGAGTTAAAGAGATGTAGAAAGTCTTACCTGCTAGGTTGAACAAATCTGAGAGTGAATACAGTG
|||||
GAAGAGTTAAAGAGATGTAGAAAGTCTTACCTGCTAGGTTGAACAAATCTGAGAGTGAATACAGTG
|||||
GAAGAGTTAAAGAGATGTAGAAAGTCTTACCTGCTAGGTTGAACAAATCTGAGAGTGAATACAGTG
2310      2320      2330      2340      2350      2360      2370
2380      2390      2400      2410      2420      2430      2440
CATTCGAGAGCAATATACAAAGTGGATTTTAAAGCAAGATTTAAAGCCCTCAGTAAAGTTTCAAAAGGCA
|||||
CATTCGAGAGCAATATACAAAGTGGATTTTAAAGCAAGATTTAAAGCCCTCAGTAAAGTTTCAAAAGGCA
2380      2390      2400      2410      2420      2430      2440
2450      2460      2470      2480      2490      2500      2510      2520
GTACCTCAGGCTTTCTGAACATTTATGATGGAATTTAAGAGTGTGTAAACCATTTGCTACCTCATTAAAGCCAC
|||||
GTACCTCAGGCTTTCTGAACATTTATGATGGAATTTAAGAGTGTGTAAACCATTTGCTACCTCATTAAAGCCAC
2450      2460      2470      2480      2490      2500      2510      2520
2530      2540      2550      2560      2570      2580      2590
CAGATGATTAATGAATTTATATAATAACAGAGGCGCTTACAGCATTTGTAGTACGTAGCAGCGGGAATCTATCC
|||||
CAGATGATTAATGAATTTATATAATAACAGAGGCGCTTACAGCATTTGTAGTACGTAGCAGCGGGAATCTATCC
2530      2540      2550      2560      2570      2580      2590
CAGATGATTAATGAATTTATATAATAACAGAGGCGCTTACAGCATTTGTAGTACGTAGCAGCGGGAATCTATCC
2530      2540      2550      2560      2570      2580      2590
2600      2610      2620      2630      2640      2650      2660
TTCTTGACAGCTTACGTATGCTGCTGAGAGAGTGGGACAGAGTTCTGATTTCTCTCAGATGGTGAGA
|||||
TTCTTGACAGCTTACGTATGCTGCTGAGAGAGTGGGACAGAGTTCTGATTTCTCTCAGATGGTGAGA
2600      2610      2620      2630      2640      2650      2660
2670      2680      2690      2700      2710      2720      2730
TGCTGGACATCTAGCAGAAATATCTGAAGTATCGCCAGTTTCCCTTCCAGAGCTTGTATGATCAATAAAG
|||||
TGCTGGACATCTAGCAGAAATATCTGAAGTATCGCCAGTTTCCCTTCCAGAGCTTGTATGATCAATAAAG
2670      2680      2690      2700      2710      2720      2730
2740      2750      2760      2770      2780      2790      2800
GGGAATTTGAGGAAGCAAGCACTGGATCATTTCAATGCAAGAGGATCAGAGGATTTCTGTTTACTCTCTA
|||||
GGGAATTTGAGGAAGCAAGCACTGGATCATTTCAATGCAAGAGGATCAGAGGATTTCTGTTTACTCTCTA
2740      2750      2760      2770      2780      2790      2800
2810      2820      2830      2840      2850      2860      2870      2880
CAAGAGCTGGAGGATTTAGGTATTAACCTGCGATCTGCGACACTGTAGTATTTGCTGCTGACTGGAATC
|||||
CAAGAGCTGGAGGATTTAGGTATTAACCTGCGATCTGCGACACTGTAGTATTTGCTGCTGACTGGAATC
2810      2820      2830      2840      2850      2860      2870      2880
2890      2900      2910      2920      2930      2940      2950
CACAGATGATCTGAGGACAGCGGAGAGCTCATGAATTTGGACAGAAAGAGATTTATTTATTCGGC
|||||
CACAGATGATCTGAGGACAGCGGAGAGCTCATGAATTTGGACAGAAAGAGATTTATTTATTCGGC
2890      2900      2910      2920      2930      2940      2950
2960      2970      2980      2990      3000      3010      3020
TAGTCACAAAAGGATCAGTGAAGAAGATATTTCTGAAAGAGCAAGAGAGATGGTGTAGACCATTTAG
|||||
TAGTCACAAAAGGATCAGTGAAGAAGATATTTCTGAAAGAGCAAGAGAGATGGTGTAGACCATTTAG
2960      2970      2980      2990      3000      3010      3020
3030      3040      3050      3060      3070      3080      3090
TAATTCAGAGATTTGACAGCAGCAGGAAAGTCTTCTCATACAGGTTCAACTCCATCAAGCTCTACACCTT
|||||
TAATTCAGAGATTTGACAGCAGCAGGAAAGTCTTCTCATACAGGTTCAACTCCATCAAGCTCTACACCTT
3030      3040      3050      3060      3070      3080      3090
3100      3110      3120      3130      3140      3150      3160
TTAATAAGAGAGGATTTATCAGCTATTTTGAAGTTTGGTCTGAGGAACCTCTTTAAAGAACCTGGAAGGAG
|||||
TTAATAAGAGAGGATTTATCAGCTATTTTGAAGTTTGGTCTGAGGAACCTCTTTAAAGAACCTGGAAGGAG
3100      3110      3120      3130      3140      3150      3160
3170      3180      3190      3200      3210      3220      3230      3240
AACAGGAGCCCAAGGAATGATATAGTGAATCTTGAAGAGAGCTGAATCTCGGAAATGAGCCAGGTC
|||||
AACAGGAGCCCAAGGAATGATATAGTGAATCTTGAAGAGAGCTGAATCTCGGAAATGAGCCAGGTC
3170      3180      3190      3200      3210      3220      3230      3240
3250      3260      3270      3280      3290      3300      3310
CATTCAGCTGTAGGGATGAGTTGCTTTCACAGTTCAGGTGGGCAACTTTTCCAAATATGATGATGAAGATGATA
|||||
CATTCAGCTGTAGGGATGAGTTGCTTTCACAGTTCAGGTGGGCAACTTTTCCAAATATGATGATGAAGATGATA
3250      3260      3270      3280      3290      3300      3310
3320      3330      3340      3350      3360      3370      3380
TTTGAGTTGGAAACCAAGAAATTTCAAGAAATTTGGGAAGAAATCATCCAGAAATCCCAACGGAGAGGATAG
|||||
TTTGAGTTGGAAACCAAGAAATTTCAAGAAATTTGGGAAGAAATCATCCAGAAATCCCAACGGAGAGGATAG
3320      3330      3340      3350      3360      3370      3380
3390      3400      3410      3420      3430      3440      3450
AGGAGAGGAGAAACAGAAAAGAACTTGAAGAAATATACATGCTCCGAGGATGAGAACTGTGCAAAAACAGA
|||||
AGGAGAGGAGAAACAGAAAAGAACTTGAAGAAATATACATGCTCCGAGGATGAGAACTGTGCAAAAACAGA
3390      3400      3410      3420      3430      3440      3450
AGGAGAGGAGAAACAGAAAAGAACTTGAAGAAATATACATGCTCCGAGGATGAGAACTGTGCAAAAACAGA
3390      3400      3410      3420      3430      3440      3450
3460      3470      3480      3490      3500      3510      3520
TCAGCTTTAATGGAGTGAAGAGAGCGCATAGGAGCAGAGATATCTTGATCTGATAGTGCCTCATCA
|||||
TCAGCTTTAATGGAGTGAAGAGAGCGCATAGGAGCAGAGATATCTTGATCTGATAGTGCCTCATCA
3460      3470      3480      3490      3500      3510      3520
3530      3540      3550      3560      3570      3580      3590      3600
CAGAAAGAAACCGCCCAAAAGCGTGGAAGACCTCGAAACCATTTCTCGAGAAATATTAAGAGATTAGTG
|||||
CAGAAAGAAACCGCCCAAAAGCGTGGAAGACCTCGAAACCATTTCTCGAGAAATATTAAGAGATTAGTG
3530      3540      3550      3560      3570      3580      3590      3600
3610      3620      3630      3640      3650      3660      3670
ATGCAGAGATCAGCGGTTTATCAAGATTTACAAGAAATTTGGTGGCCCTCTGGAAGAGTTAGATGCTGTAG
|||||
ATGCAGAGATCAGCGGTTTATCAAGATTTACAAGAAATTTGGTGGCCCTCTGGAAGAGTTAGATGCTGTAG
3610      3620      3630      3640      3650      3660      3670
3680      3690      3700      3710      3720      3730      3740
CTAGAGATGCTGACTGCTGATTAATCTGAGACAGACCTTAGACCTTTGGGTGACTTACATTAATGGAT
|||||
CTAGAGATGCTGACTGCTGATTAATCTGAGACAGACCTTAGACCTTTGGGTGACTTACATTAATGGAT
3680      3690      3700      3710      3720      3730      3740
3750      3760      3770      3780      3790      3800      3810
GCATTAAGGCTTTAAAGGACAACTTCTTGACAAAGAGAGAGGAGTAGCTTGGAAAGTTAAAGGCC
|||||
GCATTAAGGCTTTAAAGGACAACTTCTTGACAAAGAGAGAGGAGTAGCTTGGAAAGTTAAAGGCC
3750      3760      3770      3780      3790      3800      3810
3820      3830      3840      3850      3860      3870      3880
CAACCTTTCCAAATCTCAGAGTGCAGGTGAATGCAAAACTAGTCTCTCAGAAAGAGAGTGGCACCAC
|||||
CAACCTTTCCAAATCTCAGAGTGCAGGTGAATGCAAAACTAGTCTCTCAGAAAGAGAGTGGCACCAC
3820      3830      3840      3850      3860      3870      3880
3890      3900      3910      3920      3930      3940      3950      3960
TCCCAATCCATTTCTCAGATCCAGAGAGGAAAGATATGTCATCCCTCCACACAGGCTGCTC
|||||
TCCCAATCCATTTCTCAGATCCAGAGAGGAAAGATATGTCATCCCTCCACACAGGCTGCTC
3890      3900      3910      3920      3930      3940      3950      3960
3970      3980      3990      4000      4010      4020      4030
ACTTCGATATAGATTGGGGTAAAGAGATGATCCCAATCTCTTAGTAGGCATCTATGAATATGGCTATGGCA
|||||
ACTTCGATATAGATTGGGGTAAAGAGATGATCCCAATCTCTTAGTAGGCATCTATGAATATGGCTATGGCA
3970      3980      3990      4000      4010      4020      4030
```

4040 4050 4060 4070 4080 4090 4100
GCTGGAAATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAAATTTTACCTGATGATCCAGACAAGA
|||||
GCTGGAAATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAAATTTTACCTGATGATCCAGACAAGA
4040 4050 4060 4070 4080 4090 4100
4110 4120 4130 4140 4150 4160 4170
AACCCAGGCAAGCAGCTACAGACCCGTCAGACTACCTCATTAATTAATTAATTAAGACCTTGAAGAA
|||||
AACCCAGGCAAGCAGCTACAGACCCGTCAGACTACCTCATTAATTAATTAATTAAGACCTTGAAGAA
4110 4120 4130 4140 4150 4160 4170
4180 4190 4200 4210 4220 4230 4240
AGGAAGCACAAGGCTTGGTGGTCAGGCAATTCGAAGAGAGGAGACAGCAAGAAATGAAGAAATGAATGA
|||||
AGGAAGCACAAGGCTTGGTGGTCAGGCAATTCGAAGAGAGGAGACAGCAAGAAATGAAGAAATGAATGA
4180 4190 4200 4210 4220 4230 4240
4250 4260 4270 4280 4290 4300 4310 4320
AGGCTTCAAAAATAAAGAGAAATAAAGAGTGAATCTTCAACCAACCCCTCAGAAAAATCTGATGAAGATG
|||||
AGGCTTCAAAAATAAAGAGAAATAAAGAGTGAATCTTCAACCAACCCCTCAGAAAAATCTGATGAAGATG
4250 4260 4270 4280 4290 4300 4310 4320
4330 4340 4350 4360 4370 4380 4390
ATGAGGAGGAGGATAACAGGTAATGAATGAATCTGAAATTAAGAGAAAAATCTAAAAAATTCATTTGC
|||||
ATGAGGAGGAGGATAACAGGTAATGAATGAATCTGAAATTAAGAGAAAAATCTAAAAAATTCATTTGC
4330 4340 4350 4360 4370 4380 4390
4400 4410 4420 4430 4440 4450 4460
TGGATCTCCAGTTTCATATTACTGCAACCAAGTGAACAGTTCCTATCTCAGAAGAATCTGAAGAATCCATC
|||||
TGGATCTCCAGTTTCATATTACTGCAACCAAGTGAACAGTTCCTATCTCAGAAGAATCTGAAGAATCCATC
4400 4410 4420 4430 4440 4450 4460
4470 4480 4490 4500 4510 4520 4530
AGAAGACATTTAGTGTGCAAGAAAGATGAGGCTGTCAAAGCAGCACTGAAACAGCTGGATAGACAG
|||||
AGAAGACATTTAGTGTGCAAGAAAGATGAGGCTGTCAAAGCAGCACTGAAACAGCTGGATAGACAG
4470 4480 4490 4500 4510 4520 4530
4540 4550 4560 4570 4580 4590 4600
AGAAGGCCCTTCTGAAGGAGCAGCTGGAACATAGGCACTGTCTAATCAAAATCGGGATCACATTA
|||||
AGAAGGCCCTTCTGAAGGAGCAGCTGGAACATAGGCACTGTCTAATCAAAATCGGGATCACATTA
4540 4550 4560 4570 4580 4590 4600
4610 4620 4630 4640 4650 4660 4670 4680
CAGATCCCTGAAGGAGTACAAAATCCCGAGCAATAAACACAGTGGAGGAAAAATTTGGATTTTGTGT
|||||
CAGATCCCTGAAGGAGTACAAAATCCCGAGCAATAAACACAGTGGAGGAAAAATTTGGATTTTGTGT
4610 4620 4630 4640 4650 4660 4670 4680
4690 4700 4710 4720 4730 4740 4750
CCAAGTTTACAGAAATTTGATGCCAGAAAGCTGCACAACTCTACAAACATGCAATCAAAAAGCCCAAGAGT
|||||
CCAAGTTTACAGAAATTTGATGCCAGAAAGCTGCACAACTCTACAAACATGCAATCAAAAAGCCCAAGAGT
4690 4700 4710 4720 4730 4740 4750
4760 4770 4780 4790 4800 4810 4820
CTCAGCAACAATGACCAAAACATTTAGCAGCAATGTGAATACACATGTAAATCAGAAATCCAGATGTGAAA
|||||
CTCAGCAACAATGACCAAAACATTTAGCAGCAATGTGAATACACATGTAAATCAGAAATCCAGATGTGAAA
4760 4770 4780 4790 4800 4810 4820
4830 4840 4850 4860 4870 4880 4890
GACTGAAGGAGACTACAAACCATGATAGTAGCAGGACAGTTATCTTCGATAGACATTTATCACAAT
|||||
GACTGAAGGAGACTACAAACCATGATAGTAGCAGGACAGTTATCTTCGATAGACATTTATCACAAT
4830 4840 4850 4860 4870 4880 4890
4900 4910 4920 4930 4940 4950 4960
CTTATGTTTCAGGAAAGATGGGGGATTTATTTGTTTATTTCTTGGTAGAAGACTCTCAAGACTTTGTT

ACCATGATCATCAAAAAGACAGGCAATCAGGAGATGCTTACAGAAAAGTCACTCCAGGAAAAGGCCATATT
|||||
ACCATGATCATCAAAAAGACAGGCAATCAGGAGATGCTTACAGAAAAGTCACTCCAGGAAAAGGCCATATT
4900 4910 4920 4930 4940 4950 4960
4970 4980 4990 5000 5010 5020 5030 5040
CAGCCTTCAGTAATGGAAGAATACAGAGACTGGGATCACTACAAACAGGACAGAGATACTACAGTATA
|||||
CAGCCTTCAGTAATGGAAGAATACAGAGACTGGGATCACTACAAACAGGACAGAGATACTACAGTATA
4970 4980 4990 5000 5010 5020 5030 5040
5050 5060 5070 5080 5090 5100 5110
GTAACATGAAAGTTAGATGACACAGGAGACAGACAGGTCAAACTGGAAGGAACTTTAAAGACA
|||||
GTAACATGAAAGTTAGATGACACAGGAGACAGACAGGTCAAACTGGAAGGAACTTTAAAGACA
5050 5060 5070 5080 5090 5100 5110
5120 5130 5140 5150 5160 5170 5180
GCCGGGTCAATTCAGATCACCGTCCCATTCAGACCACAGATACACTCAGATCACCGTTCCACTTCAGAAAT
|||||
GCCGGGTCAATTCAGATCACCGTCCCATTCAGACCACAGATACACTCAGATCACCGTTCCACTTCAGAAAT
5120 5130 5140 5150 5160 5170 5180
5190 5200 5210 5220 5230 5240 5250
ACAGCCATCAATAATCTTCAGAGATATAGATACCACTCAGACTGCAATGGACACAGAGCTTCTGGTA
|||||
ACAGCCATCAATAATCTTCAGAGATATAGATACCACTCAGACTGCAATGGACACAGAGCTTCTGGTA
5190 5200 5210 5220 5230 5240 5250
5260 5270 5280 5290 5300 5310 5320
GTGGCCGAGGTCAACCACTAGATCAGAGTCTCTTATGTTCAAGATCTCCCTTAGACACAGATCTCCAT
|||||
GTGGCCGAGGTCAACCACTAGATCAGAGTCTCTTATGTTCAAGATCTCCCTTAGACACAGATCTCCAT
5260 5270 5280 5290 5300 5310 5320
5330 5340 5350 5360 5370 5380 5390 5400
TTGAACACTCATCAGATCAAAAAGTACCTGAACATAGATGAGTAGCGGGAAGACATAACAAAGACTGA
|||||
TTGAACACTCATCAGATCAAAAAGTACCTGAACATAGATGAGTAGCGGGAAGACATAACAAAGACTGA
5330 5340 5350 5360 5370 5380 5390 5400
5410 5420 5430 5440 5450 5460 5470
CATTTCTGAGACTTCTTTAGCCATATACAGTAACACTAACACAGTAATTCCTTACATGACTTGAAGAT
|||||
CATTTCTGAGACTTCTTTAGCCATATACAGTAACACTAACACAGTAATTCCTTACATGACTTGAAGAT
5410 5420 5430 5440 5450 5460 5470
5480 5490 5500 5510 5520 5530 5540
ATGGACTGGATATTCATCAGTAGCAGTATTGTTACTCTTTCCAGGATGCAAGGTCTATTATCCCAACAGA
|||||
ATGGACTGGATATTCATCAGTAGCAGTATTGTTACTCTTTCCAGGATGCAAGGTCTATTATCCCAACAGA
5480 5490 5500 5510 5520 5530 5540
5550 5560 5570 5580 5590 5600 5610
AGAAAATATTTTGTATTTAAAGTTTATGCTGCACGTCTGCAAAATGTTGGGCACTTTTTTTTAAAGAA
|||||
AGAAAATATTTTGTATTTAAAGTTTATGCTGCACGTCTGCAAAATGTTGGGCACTTTTTTTTAAAGAA
5550 5560 5570 5580 5590 5600 5610
5620 5630 5640 5650 5660 5670 5680
ATGGAAGATGTTTACTTTTACAGGGACCTCAACACTGCCCTTTTACAGTGGATCTTACTATAAACTCTTC
|||||
ATGGAAGATGTTTACTTTTACAGGGACCTCAACACTGCCCTTTTACAGTGGATCTTACTATAAACTCTTC
5620 5630 5640 5650 5660 5670 5680
5690 5700 5710 5720 5730 5740 5750 5760
ATGCTAAAGTGGTTCAGGCTGAACAGATTAATTTGTTGTAATGAACACTTAAACACTGACCTGTG
|||||
ATGCTAAAGTGGTTCAGGCTGAACAGATTAATTTGTTGTAATGAACACTTAAACACTGACCTGTG
5690 5700 5710 5720 5730 5740 5750 5760
5770 5780 5790 5800 5810 5820 5830
CTTATGTTTCAGGAAAGATGGGGGATTTATTTGTTTATTTCTTGGTAGAAGACTCTCAAGACTTTGTT


```
|||||
AGCTATTGTAATCTGAACACAGACTTAGACGCTCTGGGAGAGATGTACATAATGGATGCAATTAAAGCGTT
750 760 770 780 790 800 810
3760 3770 3780 3790 3800 3810 3820
TAAAGGCAATTCATCTGGACACAGAAGACGAGGTAGACTTGGGAAAGTTAAAGGCCCAACGTTTCGAA
|||||
TAAATGATAATGACTTTGGTCAAGGAAGACAGGTGTAGATTGGGAAAGTTAAAGGCCCAACATTCGAA
820 830 840 850 860 870 880
3830 3840 3850 3860 3870 3880 3890 3900
TCTCAGAGTGCAGGTGAATGCAAAATAGTCTCTCAGGAAGAGCTGGCCACCCTGACACAAATCCA
|||||
TACGAGAGTGCAGGTGAATGCAAAATAGTCTCTCAGGAAGAGAGTGGCCACCCTGACATAAATCGA
890 900 910 920 930 940 950
3910 3920 3930 3940 3950 3960 3970
TTCCCTCAGATCAGAGAAAGAAAGATATGTCATCCATGCCACCAAGCGTGTCTCCTCATTCATATAG
|||||
TTCCCTCAGATCAGAGAAAGAAAGATATGTCATCCATGCCACCAAGCGTGTCTCCTCATTCATATAG
960 970 980 990 1000 1010 1020 1030
3980 3990 4000 4010 4020 4030 4040
ATTGGGTTAAGAGATGANTCCAAATCTGTTAGTGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGA
|||||
ATTGGGTTAAGAGATGANTCCAAATCTGTTAGTGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGA
1040 1050 1060 1070 1080 1090 1100
4050 4060 4070 4080 4090 4100 4110
TAAATATGATCAGATCAGCTCAGCTTAACACAGAGAGATTTTACCTGTAGTATCCAGACAAAGAACCCCGAGCAA
|||||
TAAATATGATCAGCTCAGCTTACACAGAGAGATTTTACCTGTAGTATCCAGACAAAGAACCCCGAGCTA
1110 1120 1130 1140 1150 1160 1170
4120 4130 4140 4150 4160 4170 4180
AGCAGTACAGACCCCTGCAGACTACTCTATTAATCTGAATAAGACCTTGCAGAAAGAGACACAAA
|||||
AGCAGTACAGACTCTGCAGACTACTCTATTAATCTGAATAAGACCTTGCAGAAAGAGACACAGA
1180 1190 1200 1210 1220 1230 1240
4190 4200 4210 4220 4230 4240 4250 X
GGCTCTCTGTCAGCAATTCACAGAGAGGAGACACAGAAATAGAGAAATAA---GATGAAGGCTTCAA
|||||
GACTCTGTGTCAGGCAATTCACAGAGAGGAGAAACAAAGAGTAAAGAGATAAAGCAACAAAGGCTGC
1250 1260 1270 1280 1290 1300 1310 X
4260 4270 4280 4290 4300
AAATAAAGAGAAATAAAGAGTGTCTTCCACCACACCCCTCAGAA
```

3. US-08-973-363-10 (1-6608)

US-08-973-363-32 Sequence 32, Application US/08973363

Initial Score = 111 Optimized Score = 111 Significance = -0.25
Residue Identity = 100% Matches = 111 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```
3450 3460 3470 3480 3490 3500 3510
CAAACAGATCAGCTTTAATGGGAGTGAAGGAAGACGCGTAGGACGACAGATATTTCTGGATCTGATAGTG
|||||
AGATATTTCTGGATCTGATAGTG
X
3520 3530 3540 3550 3560 3570 3580 3590
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAATATTAAG
|||||
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAATATTAAG
30 40 50 60 70 80 90
3600 X
GATTAGTGCAGAGATCAGCGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAG
|||||
GATTAGTGCAGAG
```

100 110

4. US-08-973-363-10 (1-6608)

US-08-973-363-3 Sequence 3, Application US/08973363

Initial Score = 103 Optimized Score = 115 Significance = -0.25
Residue Identity = 75% Matches = 115 Mismatches = 38
Gaps = 0 Conservative Substitutions = 0

```
4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTGCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAAATGGATCTCAGCTTAA
|||||
ATTTTACCTGATGATCCAGACA
X
4080 4090 4100 4110 4120 4130 4140
CACAGAAGATTTTACCTGATGATCCAGACAAGAACCCCGAGCAAGCTACAGACCGTGCAGACTACC
|||||
AGAAACCCCGAGGCAAAAGAGCTACAGACCAAGAAACCCCGAGCAAGCTACAGACCGTGCAGACTACC
30 40 50 60 70 80 90
4150 4160 4170 4180 4190 4200 X 4210
TCATTAATTTACTGAATAAGACCTTGCAAGAAAGAGCAACAAAGCTTGGTGGCAAGTATCCAAGA
|||||
TCATTAATTTACTGAATAAGACCTTGCAAGAAAGAGCAACAAAGCTTGGTGGTGA
100 110 120 130 140 150 X
4220 4230 4240 4250
GAAGGAAGACAAAGAAATAAGAAGATAAGATGAAGC
```

5. US-08-973-363-10 (1-6608)

US-08-973-363-34 Sequence 34, Application US/08973363

Initial Score = 101 Optimized Score = 101 Significance = -0.26
Residue Identity = 90% Matches = 101 Mismatches = 10
Gaps = 0 Conservative Substitutions = 0

```
3450 3460 3470 3480 3490 3500 3510
CAAACAGATCAGCTTTAATGGGAGTGAAGGAAGACGCGTAGGACGACAGATATTTCTGGATCTGATAGTG
|||||
AGATATTTCTGGATCTGATAGTG
X
3520 3530 3540 3550 3560 3570 3580 3590
ACTCCATCACAGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAATATTAAG
|||||
ATTCCATCTCAGAAAGAAACGCCCAAAAGCGTGAAGACCTATTTCCCGGTGAAACATTAAG
30 40 50 60 70 80 90
3600 X
GATTAGTGCATCAGAGATCAGCGCGGTTTATCAAGAGTTACAAGAAATTTGGTGGCCCTCTGGAAG
|||||
GATTAGTGCAGAG
100 110
```

6. US-08-973-363-10 (1-6608)

US-08-973-363-36 Sequence 36, Application US/08973363

Initial Score = 99 Optimized Score = 99 Significance = -0.26
Residue Identity = 89% Matches = 99 Mismatches = 12
Gaps = 0 Conservative Substitutions = 0

```
3450 3470 3480 3490 3500 3510 3520
CAGCTTTAATGGGAGTGAAGGAAGACGCGTAGGACGACAGATATTTCTGGATCTGATAGTCCATCAC
|||||
GATCTGATAGTACTCCATCTC
X
3530 3540 3550 3560 3570 3580 3590 3600
AGAAAGAAACGCCCAAAAGCGTGAAGACCTCGAACCATTCCTCGAGAAATATTAAGGATTAGTGA
```


|||||
AGAAAGAAACGACCAAGAAACGTCGACGACCAAGCACTATCCCTCGGGAGAATATTAAGGATTAGCGCA
30 40 50 60 70 80 90

3610 X 3630 3640 3650 3660
TGCAGAGATCAGCGGTTTATCATAGAGTTTACAGAAATTTGGTGGCCCTCTGGAAAGGTTAGATGCT
|||||
TGCAGAGATTAGCGGT
100 110

7. US-08-973-363-10 (1-6608)
US-08-973-363-4 Sequence 4, Application US/08973363

Initial Score = 98 Optimized Score = 111 Significance = -0.26
Residue Identity = 73% Matches = 119 Mismatches = 34
Gaps = 9 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060
ATTCCAATCTGTTAGTGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATC
|||||
ATTTTACCTGATGCCAGATA
X 10 20

4070 4080 4090 4100 4110 4120 4130
TCAGCTTAACACAGAGATTTTACCTGATGATCCAGACAGAAACCCGAGGCAAGCAGCTTACAGACCCGTG
|||||
AGAAACCCAGCGCTAAGCAGTTA-----CAGACCAAGAAACCCGAGGCTAAGCAGTTACAGACCCGTG
30 40 50 60 70 80

4140 4150 4160 4170 4180 4190 4200 X
CAGACTACCTCATTAATTAATCTGTAATAAGACCTTGAAGAAAGGAGCACAAGGCTTGCTGGCAGGCA
|||||
CAGATTACCTCATTAATTAATCTGTAATAAGACCTTGAAGAAAGGAGCACAAGGCTTGCTGGTGA
90 100 110 120 130 140 150 X

4210 4220 4230 4240 4250
ATTCCAAGAGAAGGAGCAAGAAATAAGAAGATAAGATGAAGGC

8. US-08-973-363-10 (1-6608)
US-08-973-363-5 Sequence 5, Application US/08973363

Initial Score = 94 Optimized Score = 107 Significance = -0.26
Residue Identity = 69% Matches = 107 Mismatches = 46
Gaps = 0 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTAGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATCTCAGCTTAA
|||||
ATTTTACCTGATGCCAGATA
X 10 20

4080 4090 4100 4110 4120 4130 4140
CACAGAAGATTTTACCTGATGATCCAGACAGAAACCCGAGGCAAGCAGCTACAGACCCGTCGAGACTACC
|||||
AGAAACCAACAGGCAAGCAGTTCAGACCAACCAAGAAACCAAGCAAGGCAAGCAGTTCGAGACCCGTCGAGATTACC
30 40 50 60 70 80 90

4150 4160 4170 4180 4190 4200 X 4210
TCATTAATTAATCTGAATAAGACCTTGAAGAAAGGAGCACAAGGCTTGCTGGTGGCAAGTATTCACAA
|||||
TCATTAATTAATCTGAATAAGACCTTGAAGAAAGGAGTGAAGCAAGACTTACTGGTGA
100 110 120 130 140 150 X

4220 4230 4240 4250
GAAGGAAGACAAGAAATAAGAAGATAAGATGAAGGC

9. US-08-973-363-10 (1-6608)
US-08-973-363-2 Sequence 2, Application US/08973363

Initial Score = 94 Optimized Score = 96 Significance = -0.26

Residue Identity = 62% Matches = 96 Mismatches = 57
Gaps = 0 Conservative Substitutions = 0

4000 4010 4020 4030 4040 4050 4060 4070
TGTTAGTAGGCATCTATGAATATGGCTATGGCAGCTGGGAAATGATAAAATGGATCCAGATCTCAGCTTAA
|||||
ATTCTTCAGATGATCCTGATA
X 10 20

4080 4090 4100 4110 4120 4130 4140
CACAGAAGATTTTACCTGATGATCCAGACAGAAACCCGAGGCAAGCAGCTACAGACCCGTCGAGACTACC
|||||
AAAAACCAACAGCAAGCAAGTTCAGACACCAAAACCAAGCAAGCAGTTACAGACCCGTCGAGACTACC
30 40 50 60 70 80 90

4150 4160 4170 4180 4190 4200 X 4210
TCATTAATTAATCTGAATAAGACCTTGAAGAAAGGAGCACAAGGCTTGCTGGTGGCAAGTATTCACAA
|||||
TCATCAACTACTTACGAGAGATCTTGCACAAAGAGAGGCTCAGAGACTTTGTGTGGC
100 110 120 130 140 150 X

4220 4230 4240 4250
GAAGGAAGACAAGAAATAAGAAGATAAGATGAAGGC

10. US-08-973-363-10 (1-6608)
US-08-973-363-12 Sequence 12, Application US/08973363

Initial Score = 94 Optimized Score = 115 Significance = -0.26
Residue Identity = 45% Matches = 120 Mismatches = 144
Gaps = 1 Conservative Substitutions = 0

4030 4040 4050 4060 4070 4080 4090
ATGCTATGGCAGCTGGGAATGATAAAATGGATCCAGATCTCAGCTTAACACAGAGATTTTACCTGATG
|||||
GATGAGATTTGTTTCAGTGAAC
X 10 20

4100 4110 4120 4130 4140 4150 4160
ATCCAGACAGAAACCCGAGGCAAGCAGCTACAGACCCGTCGAGACTACCTCATTAATTAATTAAG
|||||
ATCTACATAAAATAAAACAGAAAGAAATGAAGAAAGCCCTGAGCCAGATTTGGTATATAAGAAAG
30 40 50 60 70 80 90

4170 4180 4190 4200 4210 4220 4230
ACCTTGAAGAAAGGAGCACAAGGCTTGCTGGCAGGCAATTCCA-AGAGAGGAGACAGCAATAAG
|||||
GAAGCTGAAGAAAGAGAGACACAAAGAGAAATAAAAGGGAATTGAAAGGGGAGAAAGAAAGAA
100 110 120 130 140 150 160

4240 4250 4260 4270 4280 4290 4300
AAGAAATAGATGAAGGCTTCAAAATTAAGAAAGCAATTAAGAGCTGATCTTCCACCAACCCCTCAGAAAA
|||||
GAGATTAAGAAAGATTAAGAAAGAAAGATTAAGAAAGAGAGAAACAAAGTAAAGATCCACACAG
170 180 190 200 210 220 230

4310 4320 4330 X 4340 4350 4360 4370
TCTGATCAAGATGATGAGGAGGAGATAACAAGCTAAATGAATGAATCTGAAATAAGAAAAATCTAA
|||||
AAGAAAAAGAGTGAAGGAAGAG
240 250 260 X

4380
AAAAAT

11. US-08-973-363-10 (1-6608)
US-08-973-363-31 Sequence 31, Application US/08973363

Initial Score = 91 Optimized Score = 94 Significance = -0.26
Residue Identity = 84% Matches = 94 Mismatches = 17
Gaps = 0 Conservative Substitutions = 0


```
TGGAAAGTTAAAGCCCAACATTCCGAATACGAGGAGTGCAGGTGAATGCAAAAGCTAGTCAATTTCTCAGCA
860      870      880      890      900      910      920
580
ATATAAATT-----ACAGAAATTCATAGAAATTATTAAAGGCTGGAATAAACTCTGAGATCATCGAGTCCAC
|||      |||      |||      |||      |||      |||      |||      |||      |||      |||
AGAAGAGTTGGCACCATTGGCATAAATCGATTCTTCAGATCCAGAGAAAGGAAGAAAGATGTCTATCCCATTA
930      940      950      960      970      980      990      1000
650      660      670      680      690      700      710
TTTGTCCCAACCATCACCTTGTCACTAGACCATGGCCACTAAGTCCACATCTAGTCATTCCTTGAACCTC
|||      |||      |||      |||      |||      |||      |||      |||      |||      |||
CCACACAAAGCAGCTCATTTGATATAGATTTGGGTAAAGAGATGATTCCTCATCTGTAAATAGGCATCTA
1010     1020     1030     1040     1050     1060     1070
720 X
CGACCGGG
|||
TGAATATGGTTATGGCAGTTGGGAATGATAAAAATGGATCCTGTGATCTCAGTTTGACA
1080     1090     1100     1110     1120     1130
```


[illegible]

26-03-08 9/5-363-102 (2,3008)
 NS-08-973-363-1 Sequence 1, Application US/08973363

Initial Score	=	64	Optimized Score	=	257	Significance	=	1.26
Residue Identity	=	388	Matches	=	286	Mismatches	=	432
Gaps	=	19	Conservative Substitutions	=			=	0

3. US-08-973-363-10' (1-6608)
US-08-973-363-13 Sequence 13, Application US/08973363

Initial score	-	84	Optimized score	=	257	Significance	=	1.26
Residue Identity	-	38%	Matches	=	286	Mismatches	=	432
Gaps	-	19	Conservative Substitutions	=	0			

Initial Score	=	51	Optimized Score	=	63
Residue Identity	=	48%	Matches	=	69
Gaps	=	4	Conservative Substitutions	=	

[illegible][illegible]

570 580 X 600 610 620 630
TACAGCCATTGTGGTTGTGTGTTTTTAAATGTTTGTGTTGTTGTTTCATAAAAA
||| |||
TAAGGATTAGTCACAG
90 100 110

10. US-08-973-363-10' (1-6608)

US-08-973-363-5 Sequence 5, Application US/089733363

Initial Score	=	23	Optimized Score	=	56	Significance	=	-0.36
Residue Identity	=	39%	Matches	=	61	Mismatches	=	92
Gaps	=	1	Conservative Substitutions	=			=	0

380 390 400 410 420 X 430 440
GTATCAATAAAAAAGAGCAGCTAAATGGAATAAATATCCCTCCCATTTTTCACATTCTGATTTCATCGG
ATTTTCTCCTGATGACCCGATA
X 10 20

[illegible]

GCCAAAAGAACCGCTGCGGGAAAAAGCTCATTTAATTAATTACAAATAATTCACGACCATTCTTGTTGGTTTTG
CCTCATTTAATTAATCTGAATAAAGCACTTGCAGGAAAAAGGTGCCAAAGACTTACTCTGGTGCA

590 600 610 620
TTGTGTTTTTTTTTTAATGTTTTTTTGTGTTGTTGTT

11. US-08-973-363-10' (1-6608)

US-08-973-363-36 Sequence 36, Application US/089733363

Initial Score	=	21	Optimized Score	=	43	Significance	=	-0.43
Residue Identity	=	38%	Matches	=	43	Mismatches	=	68
Gaps	=	0	Conservative Substitutions	=	0		=	0

GCACCTGAAAGACTTTTCCAGGGCACAGTTTAGAGTGGGATATTCACCTGTTTCAACAACATCACACACAC
GATCTGATAGTGACTCCATCTCT
X

TGACACTTTATAGAAAAAATAAAATTAACAACCAAAACAGGTATTCTAAAGTATCCCATTAATA
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGAAAGAAACGCACAGAAGAACCTTGACGCCACCACTTCCTCGGGCAGATATTAAAGCATTTACCCA

390 400 X 410 420 430 440 450
GGACCCTAAATGGGAATAATATCCCTCCCAATTTTACATTCGTGATCCATCGAGATATTTA
| | | | |
TGCAGAGATTAGGCGGT
100 110

12. US-08-973-363-10' (1-6608)

US-08-973-363-10. (I-6608)
US-08-973-363-33 Sequence 33, Application US/089733363

Initial Score	-	19	Optimized Score	-	31	Significance	-	-0.51
Residue Identity	-	46%	Matches	-	31	Mismatches	-	36
Gaps	-	0	Conservative Substitutions	-			-	0

450 460 470 480 490 X 500 510
ATATTTTATTAACATGTAAGTATACTGACTTTTGTGAAGAAGGCGTGACTTGTGGGAAAGGAACAGC

520 530 540 550 560 X 570 580
 CAAAAAAGCCCTGACGGAAAAAGCTCATTTAAATTAATTTACAAATAATTTACAGCCATTTGTGGTTTGTGTT
 CAAAAAAGCGTGGGAAGACCAAGCAATATTTCTCGAGAAAAATATA
 30 40 50 60 X
 590 600 610
 CCGTTTTTTTTTTTAAATGTTTT

13. US-08-973-363-10' (1-6608)

US-08-973-363-34 Sequence 34, Application US/089733363

Initial Score	=	19	Optimized Score	=	44	Significance	=	-0.51
Residue Identity	=	39%	Matches	=	44	Mismatches	=	67
Gaps	=	0	Conservative Substitutions	=	0		=	0

3670
TAACCTCTTCTTCTGTCCTCAATCTATGAGCTCGCCTGCTGCAGATCATCTGTGTGGATTCAGTCAG
3680
3690
3700
3710
3720
3730
3740
AGATAATTCGGATCTGATGATG
||| ||||| |
||| ||||| |

[illegible]

3820 x 3840 3850 3860 3870
AACAGAAACCTCTGCATTCCTTGCATTGAATCATCCAGTGCTGCTTCCCAATCCCCCTTTAT
| | | |
GATTTAGTGATGCAGAG
100 110

14. US-08-973-363-10' (1-6608)

US-08-973-363-31 Sequence 31, Application US/08973363

```
Initial Score = 17 Optimized Score = 39 Significance = -0.59
Residue Identity = 35% Matches = 39 Mismatches = 72
Gaps = 0 Conservative Substitutions = 0
```

[illegible]

2180 2190 2200 2210 2220 2230 2240
TAGGAACGTGTCACGTGGTCCAGTATATGACGTGGNGATCCAGCAATGGAATTTTTTAGATTTTCTT
ATTCAATCTCGGAAGGAAAGCGCCGCAAGAAACGTGGCGACCCCGACACTCCCTCGGGAATATTAAAG

2250 X 2270 2280 2290 2300 2310
TATTTTCAGATTTCATTTCATTTCCTGTTATCCTCCTCCTCATCTTCATCAGATTTTCTGA
|||||
GATTTAGTATGCGGAG
100 110

